Amendments to the Specification

On page 5, lines 16-25, please **delete** the paragraph beginning "[s]imilarity analysis includes database...." and replace it with the following paragraph.

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ)**(www-ddbj.nig.ac.jp/)** ~~(http://www.ddbj.nig.ac.jp/)~~; Genebank **(www-ncbi.nlm.nih.gov/web/Genbank/ Index.html)** ~~(http://www.ncbi.nlm.nih.gov/web/Genbank/Index.htlm)~~; and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) **(www-ebi.ac.uk/ebi docs/embl db.html)**~~(http://www.ebi.ac.uk/ebi docs/embl db.html)~~. A number of different search algorithms have been developed, one example of which are the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designed for nucleotide sequences queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology, 12:*76-80 (1994); Birren *et al., Genome Analysis, 1:*543-559 (1997)).

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On page 7, lines 7-24, please **delete** the paragraph beginning "[h]omologues in other organisms...." and replace it with the following paragraph.

Homologues in other organisms are available that can be used for comparative sequence analysis. Multiple alignments are performed to study similarities and differences in a group of related sequences. CLUSTAL W is a multiple sequence alignment package available that performs progressive multiple sequence alignments based on the method of Feng and Doolittle, *J. Mol. Evol.*, 25:351-360 (1987), the entirety of which is herein incorporated by reference. Each pair of sequences is aligned and the distance between each pair is calculated; from this distance matrix, a guide tree is calculated, and all of the sequences are progressively aligned based on this tree. A feature of the program is its sensitivity to the effect of gaps on the alignment; gap

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penalties are varied to encourage the insertion of gaps in probable loop regions instead of in the middle of structured regions. Users can specify gap penalties, choose between a number of scoring matrices, or supply their own scoring matrix for both the pairwise alignments and the multiple alignments. CLUSTAL W for UNIX and VMS systems is available at: **ftp-ebi.ac.uk** ~~ftp.ebi.ac.uk~~. Another program is MACAW (Schuler *et al.*, *Proteins, Struct. Func. Genet,* 9:180-190 (1991), the entirety of which is herein incorporated by reference, for which both Macintosh and Microsoft Windows versions are available. MACAW uses a graphical interface, provides a choice of several alignment algorithms, and is available by anonymous ftp at: **ncbi-nlm.nih.gov** ~~ncbi.nlm.nih.gov~~(directory/pub/macaw).

On page 28, line 22 through page 29, line 2, please **delete** the paragraph beginning "[a] PCR probe is a nucleic acid..." and replace it with the following paragraph.

A PCR probe is a nucleic acid molecule capable of initiating a polymerase activity while in a double-stranded structure with another nucleic acid. Various methods for determining the structure of PCR probes and PCR techniques exist in the art. Computer generated searches using programs such as Primer3 (available on the World Wide Web at ~~www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi~~ **genome.wi.mit.edu/cgi-bin/primer/primer3.cgi**), STSPipeline (available on the World Wide Web at ~~www-genome.wi.mit.edu/cgi-bin/www-STS_Pipleine~~ **genome.wi.mit.edu/cgi-bin/www-STS_Pipleine**) or GeneUp (Pesole *et al.*, *BioTechniques, 25*:112-123 (1998) the entirety of which is herein incorporated by reference), for example, can be used to identify potential PCR primers.

On page 55, lines 8-17, please **delete** the paragraph beginning "[a] microarray-based method..." and replace it with the following paragraph.

A microarray-based method for high-throughput monitoring of gene expression may be utilized to measure expression response Schena *et al., Science* 270: 467-470 (1995); **cmgm-stanford.edu/pbrown/array.html;** ~~http://cmgm.stanford.edu/pbrown/array.html;~~ Shalon, Ph.D. Thesis, Stanford University (1996). This approach is based on using arrays of DNA targets (*e.g.*, cDNA inserts, colonies, or polymerase chain reaction products) for hybridization to a "complex probe" prepared with RNA extracted from a given cell line or tissue. The probe may be produced by reverse transcription of mRNA or total RNA and labeled with radioactive or fluorescent labeling. The probe is complex in that it contains many different sequences in various amounts, corresponding to the numbers of copies of the original mRNA species extracted from the sample.

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